

Figure 1  
Nucleotide Sequence and predicted protein for HLTDG74

	10	30	50	
-88	GTTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29			
	70	90	110	
-28	CCCTGCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGTCGCTCCACGTCT			31
-8	M A W L G A S L H V W			11
	130	150	170	
32	GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA			91
12	G W L M L G S C L L A R A Q L D S D G T			31
	190	210	230	
92	CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCGAAAGTACAATGTGAAGTCA			151
32	I T I E E Q I V L V L K A K V Q C E L N			51
	250	270	290	
152	ACATCACAGCTCAACTCCAGGAGGGAGAAAGGTAATTGTTTCCCTGAATGGGATGGACTCA			211
52	I T A Q L Q E G E G N C F P E W D G L I			71
	310	330	350	
212	TTTGTTGGCCAGAGGAACAGTGGGGAAATATCGGCTGTTCCATGCCCTCCTTATATTT			271
72	C W P R G T V G K I S A V P C P P Y I Y			91
	370	390	410	
272	ATGACTTCAACCATAAAGGAGTTGCTTTCGACACTGTAACCCCAATGGAACATGGGATT			331
92	D F N H K G V A F R H C N P N G T W D F			111
	430	450	470	
332	TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTCTGCAGC			391
112	M H S L N K T W A N Y S D C L R F L Q P			131
	490	510	530	
392	CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG			451
132	D I S I G K Q E F C E R L Y V M Y T V G			151
	550	570	590	
452	GCTACTCCATCTCTTTGGTTCCTTGGCTGTGGCTATTCTCATCATTGGTTACTTCAGAC			511
152	Y S I S F G S L A V A I L I I G Y F R R			171
	610	630	650	
512	GATTGCATTGCACTAGGAACTATATCCACATGCACTTATTTGTGTCTTTCATGCTGAGAG			571
172	L H C T R N Y I H M H L F V S F M L R A			191
	670	690	710	
572	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG			631
192	T S I F V K D R V V H A H I G V K E L E			211

FIGURE 1 1/3

632	730	750	770	691
212	AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT			231
	S L I M Q D D P Q N S I E A T S V D K S			
692	790	810	830	751
232	CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTTATTTACTTCCTGGCTACAAATT			251
	Q Y I G C K I A V V M F I Y F L A T N Y			
752	850	870	890	811
252	ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTTT			271
	Y W I L V E G L Y L H N L I F V A F F S			
812	910	930	950	871
272	CGGACACCAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG			291
	D T K Y L W G F I L I G W G F P A A F V			
872	970	990	1010	931
292	TTGCAGCATGGGCTGTGGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACTTAGTG			311
	A A W A V A R A T L A D A R C W E L S A			
932	1030	1050	1070	991
312	CTGGAGACATCAAGTGGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA			331
	G D I K W I Y Q A P I L A A I G L N F I			
992	1090	1110	1130	1051
332	TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAATCTGGGAGACCAATGCAGTTG			351
	L F L N T V R V L A T K I W E T N A V G			
1052	1150	1170	1190	1111
352	GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCCTGGTCCTAG			371
	H D T R K Q Y R K L A K S T L V L V L V			
1112	1210	1230	1250	1171
372	TCTTTGGAGTGCATTACATCGTGTTCGTGTGCCTGCCTCACTCCTTCACTGGGCTCGGGT			391
	F G V H Y I V F V C L P H S F T G L G W			
1172	1270	1290	1310	1231
392	GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGTCTA			411
	E I R M H C E L F F N S F Q G F F V S I			
1232	1330	1350	1370	1291
412	TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			431
	I Y C Y C N G E V Q A E V K K M W S R W			
1292	1390	1410	1430	1351
432	GGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGAGATGCGGCTCAG			451
	N L S V D W K R T P P C G S R R C G S V			
1352	1450	1470	1490	1411
452	TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT			471
	L T T V T H S T S S Q S Q V A A A H A W			
	1510	1530	1550	

FIGURE 1 2/3

1412	GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC	1471	
472	C L S L A K L P R S P A D S L T A T S L	491	
	1570	1590	1610
1472	TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA	1531	
492	Y L A M S G V T Q S R T A S H T L S T R	511	
	1630	1650	1670
1532	GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA	1591	
512	S N K E D S G R Q R D D I L M E K P S R	531	
	1690	1710	1730
1592	GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT	1651	
532	P M E S N P D T E G	541	
	1750	1770	1790
1652	GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC	1711	
	1810	1830	1850
1712	TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA	1771	
	1870	1890	1910
1772	TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG	1831	
	1930	1950	1970
1832	TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCTCTAAATTAATGTAT	1891	
	1990		
1892	GGTATTTGCTCTGTGATTGTTCA	1914	

FIGURE 1 3/3

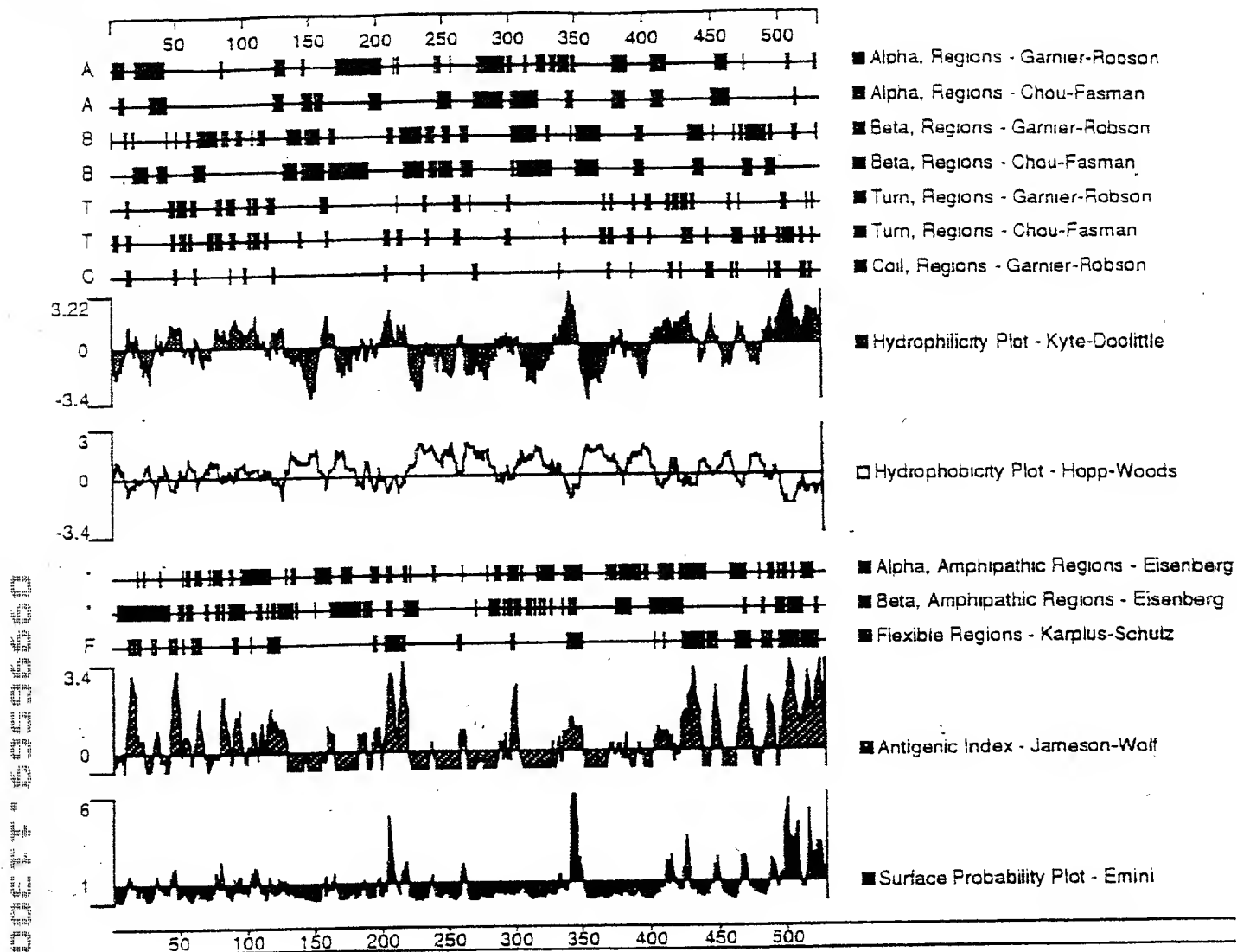


FIGURE 2 1/1

Sequences producing High-scoring Segment Pairs:      Reading      High Probability  
Fr.      Score      P(N)

gp M74445 OPOPTH_1	parathyroid hormone receptor [Di... +3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroi... +3	597	2.9e-203	6
gp L04308 HUMPTH_1	parathyroid hormone receptor [Ho... +3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h... +3	580	6.1e-189	5
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra... +3	576	7.7e-188	5
gp X78936 MMPHRPR_1	parathyroid hormone/parathyroid ... +3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr... +3	576	7.7e-188	5
gp L34611 MUSPTHRO6_1	parathyroid hormone/parathyroid ... +3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ... +3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid... +3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH\_1 parathyroid hormone receptor [Didelphis virginiana]  
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Query: 729 IMQDDPQNSIEATSVDKSKQYIGCKIAVVMFTYFLATNYWILVEGLYLHNLIFVAFFSDT 908  
I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+  
Sbjct: 253 ITEEELRAFTEPPPADKAGFVGCRVAVTVFLYFLTNYWILVEGLYLHSLIFMAFFSEK 312  
Query: 909 KYLWGFILIGWGFPAAFAAWAVARATLADARCWELSAGDIKWYQAPILAAIGLNFILE 1088  
KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF  
Sbjct: 313 KYLWGFTLFGWGLPAVFVAVVWTVRATLANTECWDLSSGNKKWLIQVPIAAIVVNFILE 372

Query: 1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVVLVLFVGVHYIVFVCLPHS 1244  
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++  
Sbjct: 373 INIIRVLATKIRETNAGRCDDTRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW 446  
+G C PEWD ++CWP G GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ + N+TW  
Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVPCPDYIYDFNHKGRAYRCDNNGSWELVPGNNRTW 161  
Query: 447 ANYSDCLRFL 476  
ANYS+C++FL  
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KOEFCEERLYVMYTVGYSSIFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677  
++E +RL ++YTVGYSSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+  
Sbjct: 177 EREVFDRLGMIYTVGYSSISLGLSLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFI 236  
Query: 678 KDRVVHAHIGVKELESIMQD 740  
KD V+++ + E+E + ++  
Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSFQGGFFVSIYCYCNGEVQAEVKKMWSRWNLSDWKRTPPCGS 1424

FIGURE 3

-G- W+++M + FNSFOGFFV+IIYC+QNGEVQAE+KK WS L++D-KF GS  
Sbjct: 427 SGILWQVQMHYLMLFNSFOGFFV+IIYCFQNGEVQAEIKKSWL LALDFKRRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLDSGTTITIEEQIVLVLKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIGURE 3